

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 00:51:17 ; Search time 6317 Seconds
(without alignments)
10798.186 Million cell updates/sec

Title: US-09-836-544C-28
Perfect score: 1200
Sequence: 1 ggggtgcaagaagacag.....aaataaagtacagatgacc 1200

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182.6	98.5	1201	6 BD015201	BD015201 Tlisa cel
2	1182.6	98.5	1204	6 AR380482	AR380482 Sequence
3	1182.6	98.5	1204	6 AX697951	AX697951 Sequence
4	1182.6	98.5	1204	6 AX818155	AX818155 Sequence
5	1182.6	98.5	1204	8 HUMCD27A	M63928 Homo sapien
6	1182.6	98.5	1323	8 BC012160	BC012160 Homo sapi
7	1181	98.4	1204	6 CQ721686	CQ721686 Sequence
8	1181	98.4	1300	6 CQ869620	CQ869620 Sequence
9	1181	98.4	1323	6 CS119000	CS119000 Sequence
10	1181	98.4	1323	6 CS119692	CS119692 Sequence
11	779.4	65.0	783	11 AY890880	AY890880 Synthetic
12	505.6	42.1	524	6 AX778265	AX778265 Sequence
13	451.8	37.6	1585	9 MUSCD27A	L24495 Mus musculu
14	435.2	36.3	1602	9 BC095844	BC095844 Rattus no
15	426	35.5	172571	8 AC006064	AC006064 Homo sapi
16	424.4	35.4	10529	8 AY504961	AY504961 Homo sapi
17	424.4	35.4	26815	6 CQ869619	CQ869619 Sequence
18	422.8	35.2	140026	8 AC005840	AC005840 Homo sapi

19	390.4	32.5	2365	8 HUMCD27AGB	L24494 Human antig
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21	361.2	30.1	516	6 CQ921958	CQ921958 Sequence
22	359.6	30.0	476	10 BV209629	BV209629 TNFRSF7.2
23	299.6	25.0	321	10 G06406	G06406 human STS.W
24	249.8	20.8	2364	8 AK056500	AK056500 Homo sapi
25	235.8	19.7	483	6 CQ070114	CQ070114 Sequence
26	235.8	19.7	483	6 CQ097846	CQ097846 Sequence
27	235.8	19.7	483	6 CQ136705	CQ136705 Sequence
28	235.8	19.7	483	6 CQ174565	CQ174565 Sequence
29	235.8	19.7	483	6 CQ220018	CQ220018 Sequence
30	235.8	19.7	483	6 CQ258428	CQ258428 Sequence
31	235.8	19.7	483	6 CQ258823	CQ258823 Sequence
32	235.8	19.7	483	6 CQ332386	CQ332386 Sequence
33	234.4	19.5	455	6 CQ079331	CQ079331 Sequence
34	234.4	19.5	455	6 CQ111004	CQ111004 Sequence
35	234.4	19.5	455	6 CQ149761	CQ149761 Sequence
36	234.4	19.5	455	6 CQ184470	CQ184470 Sequence
37	234.4	19.5	455	6 CQ233050	CQ233050 Sequence
38	234.4	19.5	455	6 CQ271024	CQ271024 Sequence
39	234.4	19.5	455	6 CQ308362	CQ308362 Sequence
40	234.4	19.5	455	6 CQ345153	CQ345153 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS BD015201 1201 bp DNA linear PAT 27-AUG-2002
DEFINITION Tlisa cell surface antigen and CD27 cell surface antigen, and utilization thereof.
ACCESSION BD015201 GI:22556008
VERSION BD015201.1
KEYWORDS JP 2001157592-A/19,
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Seed,B., Aruffo,A. and Amiot,M.
TITLE Tlisa cell surface antigen and CD27 cell surface antigen, and utilization thereof
JOURNAL Patent: JP 2001157592-A 19 12-JUN-2001;
THE GENERAL HOSPITAL CORP
COMMENT OS Homo sapiens (human)
PN JP 2001157592-A/19
PD 12-JUN-2001
PF 04-OCT-2000 JP 2000305557
PR 13-JUN-1990 US 553759
PI BRIAN SEED,ALEJANDRO ARUFFO,MARTIN AMIOT
PC C12N15/09,C07K14/725,G01N33/53,C12N15/00
CC Tlisa cell surface antigen and CD27 cell surface antigen, and utilization thereof
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FT CDS Location/Qualifiers
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FEATURES

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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 1.6e-271;
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Qy	1200	C 1200	
Db	1201	C 1201	

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RESULT 3
AX697951
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.
1
REFERENCE
AUTHORS
Lucas,J., Dyalynas,D. and Briggs,K.
TITLE
Agonists and antagonists of modumet for use in the treatment of
metabolic disorders
JOURNAL
Patent: WO 03009862-A 1 06-FEB-2003;
GENSET SA (FR)
FEATURES
source
Location/Qualifiers
1..1204
/organism="Homo sapiens"
/mol_type="unassigned DNA"

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JOURNAL	Schetzl,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,	
	Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,	
AUTHORS	Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,	
	McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	
JOURNAL	Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	
	Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,	
TITLE	Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,	
	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,	
REMARK	Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,	
	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,	
COMMENT	Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,	
	Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
PUBMED	Generation and initial analysis of more than 15,000 full-length	
	human and mouse cDNA sequences	
REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
	12477932	
JOURNAL	2 (bases 1 to 1323)	
	Strausberg,R.	
AUTHORS	Direct Submission	
	Submitted (02-AUG-2001) National Institutes of Health, Mammalian	
JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer	
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
REMARK	USA	
	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk	
	Email: cgapbs-x@mail.nih.gov	
PUBMED	Tissue Procurement: Louis Staudt	
	cDNA Library Preparation: Rubin Laboratory	
JOURNAL	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Genome Sequence Centre,	
REMARK	BC Cancer Agency, Vancouver, BC, Canada	
	info@bcgsc.bc.ca	
COMMENT	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,	
	Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth	
PUBMED	Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,	
	Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,	
JOURNAL	Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh,	
	Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska,	
REMARK	Duane Smalhus, Jeff Scott, Miranda Tsai, George Yang, Jacque	
	Schein, Asim Siddiqui, Rob Holt, Marco Marra.	
COMMENT	Clone distribution: MGC clone distribution information can be found	
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
PUBMED	Series: IRAL Plate: 29 Row: h Column: 11	
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	98.5%; Score 1182.6; DB 8; Length 1323;	
Best Local Similarity	99.6%; Pred. No. 1.6e-271;	
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LOCUS	CQ721686	1204 bp	DNA linear PAT 03-FEB-2004			
DEFINITION	Sequence 7620 from Patent WO02068579.					
ACCESSION	CQ721686					
VERSION	CQ721686.1 GI:42282543					
KEYWORDS	.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1					
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.					
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof					
JOURNAL	Patent: WO 02068579-A 7620 06-SEP-2002;					
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Query Match 98.4%; Score 1181; DB 6; Length 1204;						
Best Local Similarity 99.5%; Pred. No. 3.8e-271;						
Matches 1195; Conservative 0; Mismatches 5; Indels 1; Gaps 1;						
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Qy	1081	GCAGGAGCCACGAGCTGCGCGCGCG-TCGAGGAGGCGGGGCTCTGGTGTGAAGGCA	1139
Db	1081	GCAGGAGCCACGAGCTGCGCGCGCG-TCGAGGAGGCGGGGCTCTGGTGTGAAGGCA	1140
Qy	1140	CACCTTCTGTGTGAAAGAACCCATGCTACAGACGGGCAAAATAAAGTGCACAGATGAC	1199
Db	1141	CACCTTCTGTGTGAAAGAACCCATGCTACAGACGGGCAAAATAAAGTGCACAGATGAC	1200
Qy	1200	C 1200	
Db	1201	C 1201	
RESULT 8			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Homo sapiens (human)			
Homo sapiens			
Sequence 41 from Patent WO2004074320.			
CQ869620			
CQ869620.1			
GI:51999481			
linear			
PAT 13-SEP-2004			

RESULT 8					
CQ869620					
LOCUS				DNA	linear
DEFINITION	CQ869620	Sequence 41 from Patent WO2004074320.	1300 bp	PAT 13-SEP-2004	
ACCESSION	CQ869620				
VERSION	CQ869620.1	GI:51999481			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Db	698	GCAGCTGCTGCCCGGACTCTCTTACCCACTGGCCACCACCAAGATCCTGTGCAGCTC	757
QY	661	CGATTTTATTTGCGATCTTCTGATCTTCTGGAATGTCCTGTGTTTACCTGACCGG	720
Db	758	CGATTTTATTTGCGATCTTCTGATCTTCTGGAATGTCCTGTGTTTACCTGACCGG	817
QY	721	GGCCCTGTTCTCCATCAACGAGGAATATAGATCAAAACAAGGAGAAAGTCTGTGGA	780
Db	818	GGCCCTGTTCTCCATCAACGAGGAATATAGATCAAAACAAGGAGAAAGTCTGTGGA	877
QY	781	GCTGAGAGCTTGTGTTTACAGCTGCCCCAGGGAGGAGGGGAGAGACCATGCCCAT	840
Db	878	GCTGAGAGCTTGTGTTTACAGCTGCCCCAGGGAGGAGGGGAGAGACCATGCCCAT	937
QY	841	CCAGGAGGATTACCGAAACCGAGAGCTGCTGCTCCCTGAGCCAGCACCTGCGGTAG	900
Db	938	CCAGGAGGATTACCGAAACCGAGAGCTGCTGCTCCCTGAGCCAGCACCTGCGGGAG	997
QY	901	CTGCACTACAGCCCTGGCTCCACCCGCCACCCCGCCGACATCCAAAGGAGAGTGAGACC	960
Db	998	CTGCACTACAGCCCTGGCTCCACCCGCCACCCCGCCGACATCCAAAGGAGAGTGAGACC	1057
QY	961	TGCGAGCCCAACTGCACTGCCATCTCTGTGTCAGGGCCCTTCTCTGTGTACACGTGACA	1020
Db	1058	TGCGAGCCCAACTGCACTGCCATCTCTGTGTCAGGGCCCTTCTCTGTGTACACGTGACA	1117
QY	1021	GAGTGCCTTTTCGAGACTGGCAGGAGGAGGACAAATATGATGAGGTGGAGTGGGAA	1080
Db	1118	GAGTGCCTTTTCGAGACTGGCAGGAGGAGGACAAATATGATGAGGTGGAGTGGGAA	1177
QY	1081	GCAGGAGCCAGCAGCTGCGCGCGG-TGCAGGAGGGCGGGGCTCTGTTGTGAAGGCA	1139
Db	1178	GCAGGAGCCAGCAGCTGCGCGCTGCGCTGTCAGGAGGGCGGGGCTCTGTTGTGAAGCA	1237
QY	1140	CACTTCTCTGCTGCGAAAGCCACATGCTACAGAGCGGCAAAATAAAGTGACAGATGAC	1199
Db	1238	CACTTCTCTGCTGCGAAAGCCACATGCTACAGAGCGGCAAAATAAAGTGACAGATGAC	1297
QY	1200	C 1200	
Db	1298	C 1298	
RESULT 11			
AY890880			
LOCUS			
DEFINITION		783 bp mRNA linear SYN 21-MAR-2005	
		Synthetic construct Homo sapiens clone FLH021597.01L tumor necrosis	
		factor receptor superfamily member 7 (TNFRSF7) mRNA, partial cds.	
ACCESSION		AY890880	
VERSION		AY890880.1 GI:61366130	
KEYWORDS		Human ORF Project.	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE		1 (bases 1 to 783)	
AUTHORS		Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,	
		Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,	
		Williamson,J. and Labaer,J.	
TITLE		Cloning of human full-length CDS in Creator (TM) recombinational	
		vector system	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 783)	
AUTHORS		Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,	
		Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,	
		Williamson,J. and Labaer,J.	
TITLE		Submitted (05-JAN-2005) Biological Chemistry and Molecular	
JOURNAL		Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,	
		Cambridge, MA 02141, USA	
COMMENT		This CDS clone is a part of a collection of human full-length	
		expression clones generated by Harvard Institute of Proteomics.	
		This ORF clone has been cloned without stop-codon (to allow fusion	
		with C-terminal tag). The CDS has been directionally cloned using	

FEATURES		source	
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/db_xref="taxon:32630"			
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/lab_host="Escherichia coli DH5alpha Tl resistant"			
/note="derived from Homo sapiens first strand cDNA library			
from placenta and brain"			
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/gene="TNFRSF7"			
1..>783			
/gene="TNFRSF7"			
/codon_start=1			
/transl_table=11			
/product="tumor necrosis factor receptor superfamily			
member 7"			
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/db_xref="GI:61366131"			
/translation="MARHPWMLCVLGLSATPAKSPKPERHYWAGKLCOMCE			
PGTFLVKDCDQHRKAAQCDPCIPGVSPFDDHTRHCHSCRNCSGLLVRNCTITAGH			
ECACNKGWCRDKECTEDPLNPSTLARSQALSPQPHLPYVSEMLEARTANHM			
QTLDADFLQPLTRTHWPQRLSCSDPFIKLVIFSGMFLVFTLAGALFLHQRKYR			
SNKGSPVEPAEPKPCRYSPRBEESGSIPIQEDYQKPEPACSPL"			
ORIGIN			
Query Match		65.0%; Score 779.4; DB 11; Length 783;	
Best Local Similarity		99.9%; Pred. No. 3.2e-175;	
Matches		780; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	101	ATGGCAGCGCCACATCCCTGGTGGCTGTGCGTTCTGGGAGCCCTGGTGGGGCTCTCAGCT	160
Db	1	ATGGCAGCGCCACATCCCTGGTGGCTGTGCGTTCTGGGAGCCCTGGTGGGGCTCTCAGCT	60
QY	161	ACTCCAGCCCCCAAGAGCTGCCAGAGAGGCACTACTGGGGTTCAGGGAAAGCTGTGCTGC	220
Db	61	ACTCCAGCCCCCAAGAGCTGCCAGAGAGGCACTACTGGGGTTCAGGGAAAGCTGTGCTGC	120
QY	221	CAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACAGCATAGAAGGCTGCT	280
Db	121	CAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACAGCATAGAAGGCTGCT	180
QY	281	CAGTGTGATCCTTGTGCATACCGGGGGTCTCCTTCTCTCTGACCCACACACCGGCCCCAC	340
Db	181	CAGTGTGATCCTTGTGCATACCGGGGGTCTCCTTCTCTCTGACCCACACACCGGCCCCAC	240
QY	341	TGTGAGAGCTGTGCGGCACTGTAACTCTGGTCTTCTCGTTTCGCAACTGCACCATCACTGCC	400
Db	241	TGTGAGAGCTGTGCGGCACTGTAACTCTGGTCTTCTCGTTTCGCAACTGCACCATCACTGCC	300
QY	401	AATGCTGAGTGTGCTGTGCGCAATGGTGGCAGTGCAGGGAACAAGAGTGCACCGAGTGT	460
Db	301	AATGCTGAGTGTGCTGTGCGCAATGGTGGCAGTGCAGGGAACAAGAGTGCACCGAGTGT	360
QY	461	GATCCTCTTCCAAACCCCTTCGCTGACCGCTCGGTGCTCTCAGGCCCTGAGCCACACACCT	520
Db	361	GATCCTCTTCCAAACCCCTTCGCTGACCGCTCGGTGCTCTCAGGCCCTGAGCCACACACCT	420
QY	521	CAGCCACCCCACTTACCTTATGTCTAGTGAGATGCTTGGAGGCCAGGACAGCTGGGCACATG	580
Db	421	CAGCCACCCCACTTACCTTATGTCTAGTGAGATGCTTGGAGGCCAGGACAGCTGGGCACATG	480
QY	581	CAGACTCTGGTGTGACTTCAGGCAGTGTGCTGCCCGGACTCTCTTACCCACCTGGGCCACCC	640
Db	481	CAGACTCTGGTGTGACTTCAGGCAGTGTGCTGCCCGGACTCTCTTACCCACCTGGGCCACCC	540
QY	641	CAAAGATCCCTGTGCGAGCTCCGATTTTATTTCGATCTTGTGATCTTCTCTGGAATGTTTC	700

BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.

|||||
541 CAAAGATCCCTGTGCAGCTCCGATTTTATTTCGATCCTTTGTGATCTTCTCGAATGTTTC 600
QY CTTGTTTTCACCTCGCGCGGCTGTTCTCCATCAACGAGGAAATATAGATCAAAAC 760
Db CTTGTTTTCACCTCGCGCGGCTGTTCTCCATCAACGAGGAAATATAGATCAAAAC 660
QY AAAGGAGAAAGTCTCTGTGAGCTGCAGAGCCTTGTGTTTACAGCTGCCCCAGGAGGAG 820
Db AAAGGAGAAAGTCTCTGTGAGCTGCAGAGCCTTGTGTTTACAGCTGCCCCAGGAGGAG 720
QY GAGGCGAGCACATCCCATCCAGGAGGATTACGAAACCGAGAGCTGCTGCTCCCC 880
Db GAGGCGAGCACATCCCATCCAGGAGGATTACGAAACCGAGAGCTGCTGCTCCCC 780
QY 881 T 881
Db 781 T 781
RESULT 12
LOCUS AX778265 524 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 422 from Patent WO03039443.
ACCESSION AX778265
VERSION AX778265.1 GI:32695259
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
Dugas, M., Ellis, R., Brors, B. and Mergenthaler, S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 422 15-MAY-2003;
Deutsches Krebsforschungszentrum (DK) ;
Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES
source
1. 524
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 42.1%; Score 505.6; DB 6; Length 524;
Best Local Similarity 99.0%; Pred. No. 8.1e-110;
Matches 519; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY CTTGTGAGCTCGGATTTTATTCGATCCTTTGTGATCTTCTCGAATGTTTCTTTT 708
Db CTTGTGAGCTCGGATTTTATTCGATCCTTTGTGATCTTCTCGAATGTTTCTTTT 60
QY CACCTGGCGGGGCTGTTCTCCATCAACGAGGAAATATAGATCAAAACGAGGAG 768
Db CACCTGGCGGGGCTGTTCTCCATCAACGAGGAAATATAGATCAAAACGAGGAG 120
QY AAGTCTGTGAGGCTGCAGAGCTTGTCTGTTTACAGTGCCTCCAGGAGGAGGAGG 828
Db AAGTCTGTGAGGCTGCAGAGCTTGTCTGTTTACAGTGCCTCCAGGAGGAGGAGG 180
QY CACCATCCCATCCAGGAGGATTACCGAAACCGAGGCTGCTGCTCCCTGAGCCAG 888
Db CACCATCCCATCCAGGAGGATTACCGAAACCGAGGCTGCTGCTCCCTGAGCCAG 240
QY CACTGCGGTAGCTGACTACAGCCCTGGCTCCACCCCGCCAGCCATCCCAAGG 948
Db CACTGCGGTAGCTGACTACAGCCCTGGCTCCACCCCGCCAGCCATCCCAAGG 300
QY GAGAGTGCAGACCTGGCAGGCACAACTGCAGTCCCATCTCTTGTTCAGGGCCCTTTCCTGT 1008
|||||

301 GAGAGTGAGACCTGGCAGCCACAACTGCAGTCCCATCTTGTTCAGGGCCCTTTCTCTGT 360
QY 1009 GTACACGTGCACAGAGTGCCTTTTCGAGACTGCAGGACGAGACAAAATATGATGAGGT 1068
Db 361 GTACACGTGCACAGAGTGCCTTTTCGAGACTGCAGGACGAGACAAAATATGATGAGGT 420
QY 1069 GGAGAGTGGGAAGCAGGAGCCCGAGCAGCTGCGCGCGG- TGCAGAGGCGCGGGCTCT 1127
Db 421 GGAGAGTGGGAAGCAGGAGCCCGAGCAGCTGCGCGCTGCGCTGCAGAGGCGCGGGCTCT 480
QY 1128 GCTTGTAGGCACTTCTCTGCTGCGAAGACCCACATGCTACA 1171
Db 481 GCTTGTAGGCACTTCTCTGCTGCGAAGACCCACATGCTACA 524
RESULT 13
LOCUS MUSCD27A 1585 bp mRNA linear ROD 25-SEP-1993
DEFINITION Mus musculus CD27 antigen (cd27) mRNA.
ACCESSION L24495
VERSION L24495.1 GI:403146
KEYWORDS CD27 antigen.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Gravestein, L.A., Blom, B., Nolten, L.A., de Vries, E., van der
Horst, G., Ossendorp, F., Borst, J. and Loenen, W.A.
TITLE Cloning and expression of murine CD27: comparison with 4-1BB,
another lymphocyte-specific member of the nerve growth factor
receptor family
JOURNAL Eur. J. Immunol. 23 (4), 943-950 (1993)
PUBMED 8384562
COMMENT Original source text: Mus musculus (strain B6/CBAF1J) (library:
oligo dT in lambda ZAP) female Juvenile, 6-8 weeks thymus cDNA to
mRNA.
FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/sex="female"
/tissue_type="thymus"
/dev_stage="Juvenile, 6-8 weeks"
/tissue_lib="oligo dT in lambda ZAP"
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Query Match 37.6%; Score 451.8; DB 9; Length 1585;
Best Local Similarity 73.2%; Pred. No. 5e-97;
Matches 633; Conservative 0; Mismatches 202; Indels 30; Gaps 3;
QY GGCACAGAAAGGAGCGCTGGCAGGACCAATGACCGGCCACATCCCTGCTGCTGT 128
Db 146 GGCCTCAGAAAGATCTCCCTGGCAGGAGCTATGTCATGGCCACCTCTACTGGCTCT 205
QY 129 GCCTTCTGGGACCTGTTGGGCTCTCAGCTACTCCAGCCCCAGAGCTGCCAGAGA 188
Db 206 GCATGCTGGGACCTTGGTAGGACTCTCAGCTACCTAGCCCTCAACAGCTGTCCAGACA 265
QY 189 GGCACCTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCAGGAACATTCCTCG 248
Db 266 AACCTACTGAGCTGGGGAGGACTCTGCTCCGGATGTGTGAGCCAGGTACATCTTTG 325
QY 249 TGAAGGACTGTGACCAAGCATAGAAAGCTGCTCAGTGTGATCTTGTGATATCCGGGGTCT 308
Db 326 TGAAGGACTGTGAAACAAGACAGAAACAGCTGCTCAGTGTGATCTCTGTATACAGGCACCT 385
QY 309 CTTTCTCTCTGACCAACACACCCGGGCCCTGCTGTGAGAGCTGTGCGACATGTAACCTG 368
Db 386 CTTTCTCTCAGACTACCAACCCGGGCCCTGCTGCGAGAGCTGCGAGGACTGTGAACCTG 445
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QY	369	GTCTTCTCGTTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTGCGCAATGGCT	428
Db	446	GTITTTCTTATCCGAACTGCACAGTCACTCCCAATGCTGAGTGCAGCTGTTCAGAACT	505
QY	429	GGCAGTGCAGGGCAAGAGAGTGCACCGAGTGTGATCTCTTCCAAACCCCTTCGCTGACCG	488
Db	506	GGCAGTGCAGGACCAAGGAATGACAGAGTGTGACCTCTCTTAACCCCTGCACTGACCA	565
QY	489	CTCGTGTCTTCAGGCGCTGAGCCCAACCTCAGGCCACCACTTACCTTATGTCAAGTG	548
Db	566	GACAGGCATCTGAGACCCCGAGCCCAAGCCACCACTTACCTTATGTGACAG	625
QY	549	AGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGGCTGACTTCAGGCACCTGC	608
Db	626	AGAGC-----CATCTGGCCCTTCA-----CAGGCACCTTC	658
QY	609	CTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGCGAGCTCCGATTTTA	668
Db	659	CCAACTCGACTGTCTATAGCAGCGGTCACTCCATAGACCCCTGTGCAGCTCGGACTGCA	718
QY	669	TTGCGATCCTTGTGATCTTCTCGGAATGTTCTCTGTTTTCACCTTGGCGGGGCCCTGT	728
Db	719	TCCGATCTTTGTGACCTTCTCCAGCATGTTTCTTATCTTCTGCTGGGTGCAATCTTGT	778
QY	729	TCTCTCATCAACGAAGAAATATAGATCAAAAGGAGAAAGTCTCTGTGGAGCCTGCAG	788
Db	779	TCTTCCATCAAGAGAAACACCGGCCA---AATGAAGACCGGAGGAGTGCCTGGAAG	835
QY	789	AGCTTTGTCTTACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	848
Db	836	AGCTTTGTCTTACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	895
QY	849	ATTACCGAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	908
Db	896	ACTACCGGAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	955
QY	909	CAGCCCTGGCTCCACCCACCC 933	
Db	956	ACGAGGGCCATCCACAGAGACCTC 980	
RESULT 14			
BC095844			
LOCUS			
DEFINITION	Rattus norvegicus similar to CD27 antigen precursor - mouse, mRNA		
ACCESSION	BC095844		
VERSION	BC095844.1		
KEYWORDS	MGC.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM			
REFERENCE			
AUTHORS			

CONSRTM
TITLE
JOURNAL
PUBMED
AUTHORS
CONSRTM
TITLE
JOURNAL
REMARK
COMMENT

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1602)
NIH MGC Project
Direct Submission
Submitted (06-MAY-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 227 Row: C Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.

FEATURES
source

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/clone="MGC:112688 IMAGE:7389613"
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LPDSTVYSELSPQRECLSDSCLIRIFVTFSSMLLVFLGGLFFHQRNHPNEDSOAV
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gene

CDS

ORIGIN

Query Match	36.3%;	Score 435.2;	DB 9;	Length 1602;
Best Local Similarity	73.4%;	Pred. No. 4.6e-93;		
Matches 611;	Conservative 0;	Mismatches 188;	Indels 33;	Gaps 3;
QY	69	GGGCACAGAAAGGAGCGCCTTGGGCAGGAGGACATGGCACGGCCACATCCCTGGTGGCTGT	128	
Db	32	GGGCTCAGAGAGCTCTCCCTGACAGGAGCCATGGCATGGCCACCCCTCTACTGGCTCT	91	
QY	129	GCGTTCGGGACCCCTGGTGGGGCTCTAGCTACTCCAGCCCCCAGAGCTGCCCAGAGA	188	
Db	92	GCATGCTGGGACCTTGGTAGGGCTCTTAGCTACCCAGCCCCAACAACTGTCCAGACA	151	
QY	189	GGCACTACTGGGCTCAGGGAAGCTGTGTGTCGCCAGATGTGTGAGCCAGGAACATTCCTCG	248	

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

FEATURES

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repeat_region
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repeat_region
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6058..6083
/rpt_family="(CCCCAG)n"
repeat_region
complement(6084..6101)
/rpt_family="L1MB7"
repeat_region
complement(6102..6412)
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repeat_region
complement(6420..6551)
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6556..6668
/rpt_family="L1ME3A"
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6885..6993
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8411..8539
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8519..8823
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10852..11158
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11303..11606
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15221..15506
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repeat_region
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Query Match 35.5%; Score 426; DB 8; Length 172571;

Best Local Similarity 98.7%; Pred.No. 4e-91; Matches 440; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 756 CAAACAAGGAGAAAGTCTGTGGAGCCTGCGAGAGCTTTGTGTACAGCTGCCCCAGG 815
DB 8383 CAGACAAGGAGAAAGTCTGTGGAGCCTGCGAGAGCTTTGTGTACAGCTGCCCCAGG 8442
QY 816 AGGAGAGGGCAGCACCATCCCCATCCAGGAGGATTACGAAACCGGAGCCTGCTGCT 875
DB 8443 AGGAGAGGGCAGCACCATCCCCATCCAGGAGGATTACGAAACCGGAGCCTGCTGCT 8502
QY 876 CCCCCTGAGCCAGCACCTGCGGTAGTGCACGTACAGCCTGCGCCTCCACCCACCCCGC 935
DB 8503 CCCCCTGAGCCAGCACCTGCGGTAGTGCACGTACAGCCTGCGCCTCCACCCACCCCGC 8562
QY 936 CGACCATCCAAGGAGAGTGAGACCTGGCAGCCCAACTGCAGTCCCCTCTTTGTCTAG 995
DB 8563 CGACCATCCAAGGAGAGTGAGACCTGGCAGCCCAACTGCAGTCCCCTCTTTGTCTAG 8622
QY 996 GGCCTTTCTGTGTACAGTGACAGTGCTTTTCGAGACTGGCAGGAGCAGGACAA 1055
DB 8623 GGCCTTTCTGTGTACAGTGACAGTGCTTTTCGAGACTGGCAGGAGCAGGACAA 8682
QY 1056 ATATGATGAGTGAGAGTGGAAGCAGGAGCCAGCAGCTGCGCGCG-TGCAGGA 1114
DB 8683 ATATGATGAGTGAGAGTGGAAGCAGGAGCCAGCAGCTGCGCGCTGCGCTGAGGA 8742
QY 1115 GGGCGGGGCTCTGGTTGTAAAGGCACATCTTCTGTGCGAAAGACCAATGCTACAAGA 1174
DB 8743 GGGCGGGGCTCTGGTTGTAAAGGCACATCTTCTGTGCGAAAGACCAATGCTACAAGA 8802
QY 1175 CGGGAAAATAAAGTGACAGATGACC 1200
DB 8803 CGGGAAAATAAAGTGACAGATGACC 8828

Search completed: December 7, 2005, 06:01:41
Job time : 6324 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 00:47:12 ; Search time 810 Seconds
(without alignments)
9873.619 Million cell updates/sec

Title: US-09-836-544C-28

Perfect score: 1200

Sequence: 1 ggggtgcaagaagacg.....aaataaagtacagatgacc 1200

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1200	100.0	1200	2	AAV63459 Human CD2
2	1200	100.0	1200	2	AAV81216 Human CD2
3	1200	100.0	1200	4	AAV81216 Human T-1
4	1200	100.0	1200	12	AAO49368 Human CD2
5	1200	100.0	1200	2	AAQ21183 Encodes T
6	1196.8	99.7	1200	2	AAQ21183 Human cel
7	1196.8	99.7	1200	3	AAQ50595 Human cel
8	1182.6	98.5	1204	8	ABQ80112 Modumet c
9	1182.6	98.5	1204	8	ACB64893 Human CD2
10	1182.6	98.5	1204	10	ADD25535 Binding d
11	1182.6	98.5	1204	10	ADL15014 Human T-c
12	1182.6	98.5	1204	11	ADL131701 Human cdn
13	1182.6	98.5	1204	12	ADQ19552 Human sof
14	1182.6	98.5	1204	13	ADQ83768 Human lym
15	1182.6	98.5	1711	12	ADQ23741 Human sof
16	1181	98.4	1300	13	ABD32559 Human can
17	1181	98.4	1323	12	ADP10460 Reference
18	1179.4	98.3	1204	13	ADQ85319 Human tum
19	1179.4	98.3	1204	13	ACF87472 Human SIR

20	1057.4	88.1	1479	13	ACN42265	Acn42265 Human dia
21	783	65.2	783	14	ADV43499	Adv43499 Human psy
22	731.4	60.9	1148	13	ACN42266	Acn42266 Human dia
23	564.8	47.1	622	14	ACL60681	ACL60681 Human col
24	518.6	43.2	892	4	AAI85846	AAI85846 Human pol
25	505.6	42.1	524	10	ADF79866	ADF79866 Leukaemia
26	426	35.5	172570	6	ABQ88207	ABQ88207 Human ost
27	424.4	35.4	26815	13	ABD32558	ABD32558 Human can
28	369.4	30.8	1290	13	ABD32557	ABD32557 Mouse can
29	361.2	30.1	516	13	ADU12719	ADU12719 Solid tum
30	235.8	19.7	483	4	AAI15981	AAI15981 Probe #59
31	235.8	19.7	483	4	ABAS8384	ABAS8384 Human foe
32	235.8	19.7	483	4	AAI38019	AAI38019 Probe #67
33	235.8	19.7	483	4	ABA27495	ABA27495 Probe #59
34	235.8	19.7	483	4	AAK32170	AAK32170 Human bon
35	235.8	19.7	483	4	AAK06489	AAK06489 Human bra
36	235.8	19.7	483	4	ABQ31867	ABQ31867 Human liv
37	235.8	19.7	483	6	ABQ06937	ABQ06937 Human gen
38	234.4	19.5	455	4	AAI25198	AAI25198 Probe #15
39	234.4	19.5	455	4	ABA70980	ABA70980 Human foe
40	234.4	19.5	455	4	AAI51177	AAI51177 Probe #19
41	234.4	19.5	455	4	ABA37400	ABA37400 Probe #15
42	234.4	19.5	455	4	AAK45226	AAK45226 Human bon
43	234.4	19.5	455	4	AAK19256	AAK19256 Human bra
44	234.4	19.5	455	4	ABSA4899	ABSA4899 Human liv
45	234.4	19.5	455	6	ABS19476	ABS19476 Human gen

ALIGNMENTS

RESULT 1	
AAV63459	
ID	AAV63459 standard; cdna; 1200 BP.
XX	AC AAV63459;
XX	XX
DT	25-MAR-2003 (revised)
DT	07-JUN-1999 (first entry)
XX	DE Human CD27 antigen cdna.
XX	XX
KW	CD27; cell surface antigen; human; T lymphocyte; cloning; ss.
XX	XX
OS	Homo sapiens.
XX	XX
PH	Key Location/Qualifiers
CDS	FT 101..883
FT	/*tag= a
FT	sig_peptide 101..160
FT	/*tag= b
FT	mat_peptide 161..880
FT	/*tag= c
XX	XX
PN	US5830731-A.
XX	XX
PD	03-NOV-1998.
XX	XX
PF	21-MAY-1997; 97US-00861205.
XX	XX
PR	25-FEB-1988; 88US-00160416.
PR	13-JUL-1989; 89US-00379076.
PR	23-MAR-1990; 90US-00498809.
PR	13-JUL-1990; 90US-00553759.
PR	01-DEC-1992; 92US-00983647.
XX	XX
PA	(GEO) GEN HOSPITAL CORP.
XX	XX
PI	Seed B, Aruffo A;
XX	XX
DR	WFI; 1998-609251/51.
XX	P-PSDB; AAW80451.
XX	XX


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PI Amiot M, Lauffer L, Allen J, Simmons D, Aruffo A;
XX WPI: 1999-069813/06.
DR P-PSDB; AAW86198.
XX
PT cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell
PT surface antigens, constructing cDNA libraries, expressing vectors for
PT expression in eukaryotic cells or their fragments.
XX
PS Example 13; Col 65-66; 79pp; English.
XX
CC This nucleotide sequence comprises human CD27 cDNA. The cDNA was isolated
CC from a human T lymphocyte cDNA library using a novel method for cloning
CC cDNAs from mammalian expression libraries. The method is based on
CC transient expression of an antigen in eukaryotic cells and physical
CC selection of cells expressing the antigen by adhesion to an antibody-
CC coated substrate. The method is useful for the isolation and molecular
CC cloning of any protein which can be expressed and transported to the cell
CC surface membrane of a eukaryotic cell. It has been used to clone genes
CC (see AAW81198-220) encoding cell surface antigens such as CD1a, CD1b,
CC CD1c, CD2, CD6, CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27,
CC CD28, CD31, CD32, CD33, CD34, CD36, CD37, CD38, CD39, CD40,
CC CD43, CD44, CD53, ICAM, LFA-3, FcR1a, FcR1b, T1a and Leu8 (see AAW86198
CC -62, AAW89151-52 and AAW88451). CD40 cDNA (see AAW81198) is specifically
CC claimed. CD27, a T lymphocyte activation antigen, has been expressed in
CC COS cells
XX
SQ Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;
Query Match 100.0%; Score 1200; DB 2; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGCAAGAGAGACAGCAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
DB 1 GGGGTGCAAGAGAGAGACAGCAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
QY 61 CAGCAACTGGGACAGAGAAAGAGCGCGCTGGGAGGACCATGGCAGCGGCACATCCCTG 120
DB 61 CAGCAACTGGGACAGAGAAAGAGCGCGCTGGGAGGACCATGGCAGCGGCACATCCCTG 120
QY 121 GTGGCTGTGGGCTTCTGGGACCCCTGGTGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180
DB 121 GTGGCTGTGGGCTTCTGGGACCCCTGGTGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180
QY 181 CCCAGAGAGGCACTACTGGGGCTCAGGGAAGCTGTGTGCCAGATGTGTAGCCAGGAAC 240
DB 181 CCCAGAGAGGCACTACTGGGGCTCAGGGAAGCTGTGTGCCAGATGTGTAGCCAGGAAC 240
QY 241 ATTCTCTGTAGGACCTGTGACCAAGCATAGAAAGGCTGCTCAGTGTGATCTTCATACC 300
DB 241 ATTCTCTGTAGGACCTGTGACCAAGCATAGAAAGGCTGCTCAGTGTGATCTTCATACC 300
QY 301 GGGGGTCTCTCTCTCTGACACCAACACCCGCGCCCTCAGTGTGAGAGCTGTGGGCACTG 360
DB 301 GGGGGTCTCTCTCTCTGACACCAACACCCGCGCCCTCAGTGTGAGAGCTGTGGGCACTG 360
QY 361 TAACCTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTG 420
DB 361 TAACCTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTG 420
QY 421 CAATGGCTGGGAGTGCAGGAGCAGAGAGTGCACCGAGTGTATCTTCCAAACCCCTTC 480
DB 421 CAATGGCTGGGAGTGCAGGAGCAGAGAGTGCACCGAGTGTATCTTCCAAACCCCTTC 480
QY 481 GCTGACCGCTCGGTCTCAGGCGCTCAGCGCCACACCCCTCAGCGCCACCCACTTACCTTA 540
DB 481 GCTGACCGCTCGGTCTCAGGCGCTCAGCGCCACACCCCTCAGCGCCACCCACTTACCTTA 540
QY 541 TGTGAGTGTGAGTGTGGAGGCCAGGACAGTGGGCACATGAGACTCTGGGTGACTTCAG 600
DB 541 TGTGAGTGTGAGTGTGGAGGCCAGGACAGTGGGCACATGAGACTCTGGGTGACTTCAG 600
601 GCAGCTGCTGCGCGGAGCTCTCTTACCCACCTGGCCACCCCAAGATCCCTGTGCAGCTC 660
601 GCAGCTGCTGCGCGGAGCTCTCTTACCCACCTGGCCACCCCAAGATCCCTGTGCAGCTC 660
661 CGATTTTATTCGATCCTTGTGATCTTCTGGAATGTTCTTGTGTTTTCACCCCTGGCCGG 720
661 CGATTTTATTCGATCCTTGTGATCTTCTGGAATGTTCTTGTGTTTTCACCCCTGGCCGG 720
721 GGCCCTGTTTCTCCATCAACGAAGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
721 GGCCCTGTTTCTCCATCAACGAAGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
781 GCTCAGAGCCTTGTGCTTACAGCTGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
781 GCTCAGAGCCTTGTGCTTACAGCTGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
841 CCAGGAGGATTAACCGAAACCGGAGGCTGCTCTCCCTCCCTGAGCCAGCAGCAGCTGCGGTAG 900
841 CCAGGAGGATTAACCGAAACCGGAGGCTGCTCTCCCTCCCTGAGCCAGCAGCAGCTGCGGTAG 900
901 CTGCACTACAGCCCTGGCTTCCACCCCGCCGACCATCAAGGGAGAGTGAAC 960
901 CTGCACTACAGCCCTGGCTTCCACCCCGCCGACCATCAAGGGAGAGTGAAC 960
961 TGGCAGCACAATGAGTCCCATCTCTTGTGAGGCGCTTCTGTGTACAGCTGACA 1020
961 TGGCAGCACAATGAGTCCCATCTCTTGTGAGGCGCTTCTGTGTGTACAGCTGACA 1020
1021 GAGTGCCTTTTCGAGACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1021 GAGTGCCTTTTCGAGACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1081 GCAGGAGCCAGCAGCTGCGCGGCTGCGAGGAGGCGGGGCTCTGTGTTGAAGGCAC 1140
1081 GCAGGAGCCAGCAGCTGCGCGGCTGCGAGGAGGCGGGGCTCTGTGTTGAAGGCAC 1140
1141 ACTTCTGTGTCGAAAGACCAATGCTACAAAGCGGGCAAAATAAAGTGCAGATGACC 1200
1141 ACTTCTGTGTCGAAAGACCAATGCTACAAAGCGGGCAAAATAAAGTGCAGATGACC 1200
RESULT 3
AAS03189
ID AAS03189 standard; cDNA; 1200 BP.
XX
AC AAS03189;
XX
XX 29-AUG-2001 (first entry)
XX
DE Human T-lymphocyte specific antigen CD27 cDNA sequence.
XX
KW Human; T-lymphocyte specific antigen; immune-mediated disease; CD27;
KW infection; immune deficiency disorder; hypersensitivity; inflammation;
KW systemic lupus erythematosus; platelet disorder; rheumatoid arthritis;
KW transplant rejection; asthma; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 101..883
XX FT /*tag= a
XX FT /product= "CD27 antigen"
XX FT /transl_except= (pos:200..202,aa:Arg)
XX FT sig_peptide 101..160
XX FT /*tag= b
XX FT mat_peptide 161..880
XX FT /*tag= c
XX
XX US6218525-B1.
XX
XX 17-APR-2001.
XX
XX 01-DEC-1992; 92US-00983647.
```

XX 25-FEB-1988; 88US-00160416.
PR 13-JUL-1989; 89US-00379076.
PR 13-JUL-1990; 90US-00553759.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
XX Seed B, Aruffo A, Simmons D;
XX
XX WPI; 2001-289848/30.
DR P-PSDB; AAU02446.
XX
XX New recombinant DNA encoding CD28 useful for diagnosing and treating
PT immune-mediated diseases, infections or disorders, e.g. systemic lupus
PT erythematosus, asthma, transplant rejection, rheumatoid arthritis.
XX
XX Example 13; Col 61-62; 72pp; English.
XX
XX The present sequence encoding for human T-lymphocyte specific antigen
CC CD27 is 1 of various human lymphocyte cell surface antigen cDNA sequences
CC (AAS03172, AAS03173, AAS03175-AAS03195) described in the present
CC invention. The invention relates to a novel method of cloning cDNA
CC encoding cell surface antigens and efficient construction of cDNA
CC libraries. Also described are 2 expression vectors (AAS03171, AAS03174)
CC which provide high level expression in eukaryotic host cells. A
CC genetically engineered cDNA sequence encoding the CD28 amino acid
CC extracellular domain sequence (amino acids 1-134 given in AAU02437)
CC and/or comprising nucleotides 100-759, 154-555 or 154-759 of the CD28
CC cDNA sequence (AAS03175) is also new. The purified genes and proteins are
CC useful for immunodiagnostic and immunotherapeutic applications, such as
CC in the diagnosis and treatment of immune-mediated diseases, infections or
CC disorders in animals and humans. Such diseases include immune deficiency
CC diseases, diseases of immediate type of hypersensitivity, asthma,
CC hypersensitivity pneumonitis, systemic lupus erythematosus, rheumatoid
CC arthritis, acute and chronic inflammation, platelet disorders, plasma and
CC other cell neoplasms, parasitic diseases, multiple sclerosis, Guillain-
CC Barre syndrome and tissue and organ transplant rejection. The sequences
CC can also be used to identify, isolate and purify other antibodies and
CC antigens
XX
SQ Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;
Query Match 100.0%; Score 1200; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGCAAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
DB 1 GGGGTGCAAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
QY 61 CAGCAACTGGGCACAGAAAGAGAGCGCCGCTGGGAGAGGACATGGGACGCGCACATCCCTG 120
DB 61 CAGCAACTGGGCACAGAAAGAGAGCGCCGCTGGGAGAGGACATGGGACGCGCACATCCCTG 120
QY 121 GTGGCTGTGGTCTCGGGACCCCTGTGGGGCTCTCAGTACTCCAGGCCCCCAAGAGCTG 180
DB 121 GTGGCTGTGGTCTCGGGACCCCTGTGGGGCTCTCAGTACTCCAGGCCCCCAAGAGCTG 180
QY 181 CCACAGAGGACACTACTGGGCTCAGGGAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
DB 181 CCACAGAGGACACTACTGGGCTCAGGGAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
QY 241 ATTCTCTGTGAAGGACTGTGACAGCATAGAAAGGCTGTCTCAGTGTGATCCTTGCATACC 300
DB 241 ATTCTCTGTGAAGGACTGTGACAGCATAGAAAGGCTGTCTCAGTGTGATCCTTGCATACC 300
QY 301 GGGGGTCTCTTCTCTCTGACACACACACCGGCCCCCTGTGAGAGCTGTGCGCACTG 360
DB 301 GGGGGTCTCTTCTCTCTGACACACACACCGGCCCCCTGTGAGAGCTGTGCGCACTG 360
QY 361 TAACTCTGGTCTTCTCTGTTGCGCACTGCAACCTCACTGCGCAATGCTGAGTGTGCTGTGCG 420
DB 361 TAACTCTGGTCTTCTCTGTTGCGCACTGCAACCTCACTGCGCAATGCTGAGTGTGCTGTGCG 420

QY 421 CAATGCTGGCAGTGCAGGGACAAGGAGTGACCGAGTGTGATCTCTTCCAAACCCCTTC 480
DB 421 CAATGCTGGCAGTGCAGGGACAAGGAGTGACCGAGTGTGATCTCTTCCAAACCCCTTC 480
QY 481 GCTGACCGCTCGGTGCTCTCAGGCCCTGAGGCCACACCCCTCAGGCCACCCACTTACTTAA 540
DB 481 GCTGACCGCTCGGTGCTCTCAGGCCCTGAGGCCACACCCCTCAGGCCACCCACTTACTTAA 540
QY 541 TGTCAAGTGTGAGTGTGGAGGCCAGGACAGTGTGGGACATGACAGATCTCTGGCTGACTTCAG 600
DB 541 TGTCAAGTGTGAGTGTGGAGGCCAGGACAGTGTGGGACATGACAGATCTCTGGCTGACTTCAG 600
QY 601 GCAGTGTCTGCTGCGGAGCTCTCTTACCCACTGGCCACCCCAAGATCTCTGTGCAAGTCC 660
DB 601 GCAGTGTCTGCTGCGGAGCTCTCTTACCCACTGGCCACCCCAAGATCTCTGTGCAAGTCC 660
QY 661 CGATTTTATTCGCATCTTGTGATCTTCTCTGGAATGTTCTTGTGTTTTCACCCCTGGCCGG 720
DB 661 CGATTTTATTCGCATCTTGTGATCTTCTCTGGAATGTTCTTGTGTTTTCACCCCTGGCCGG 720
QY 721 GGCCTGTGTTCTTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
DB 721 GGCCTGTGTTCTTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
QY 781 GCCTGACAGAGCTTGTGCTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 GCCTGACAGAGCTTGTGCTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CCAGAGGAGATTACCGAAACCGAGCTGCTGCTGCCCTCAGCCAGCAGCACCTGCGGTAG 900
DB 841 CCAGAGGAGATTACCGAAACCGAGCTGCTGCTGCCCTCAGCCAGCAGCACCTGCGGTAG 900
QY 901 CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGGACCATCCAAAGGAGAGTGTGAGACC 960
DB 901 CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGGACCATCCAAAGGAGAGTGTGAGACC 960
QY 961 TGGGAGCCCAACTGAGTGTGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 TGGGAGCCCAACTGAGTGTGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 GAGTGTGCTTTTCGAGACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 GAGTGTGCTTTTCGAGACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GCAGAGGCCAGCCAGCTGCGCGCGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GCAGAGGCCAGCCAGCTGCGCGCGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 ACTTCTGTGTCGAAGACCCACATGCTACAGAGCGGCGGCAAAATAAAGTGACAGATGACC 1200
DB 1141 ACTTCTGTGTCGAAGACCCACATGCTACAGAGCGGCGGCAAAATAAAGTGACAGATGACC 1200
RESULT 4
AD049368
ID AD049368 standard; cDNA; 1200 BP.
XX
AC AD049368;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human CD27 cDNA.
XX
KW cell surface antigen; immune-mediated disorder; asthma;
KW rheumatoid arthritis; multiple sclerosis; vasculitis; inflammation; ss;
KW gene; human.
XX
OS Homo sapiens.
XX
PN US2004072283-A1.
XX
PD 15-APR-2004.

```
XX 17-APR-2001; 2001US-00836544.
PF 25-FEB-1988; 88US-00160416.
XX 13-JUL-1989; 89US-00379076.
PR 23-MAR-1990; 90US-00498809.
PR 13-JUL-1990; 90US-00553759.
PR 01-DEC-1992; 92US-00983647.
XX (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
XX Seed B, Allen J, Aruffo A, Camerini D, Lauffer L, Oquendo C;
PI Simmons D, Stamenkovic I, Stengelin S, Amiot M;
XX P-PSDB; ADO49369.
DR WPI; 2004-328571/30.
DR
XX New cloning cDNA segments encoding cell surface antigens of human
PT lymphocytes, useful in diagnosing and treating asthma, rheumatoid
PT arthritis, multiple sclerosis, vasculitis and inflammation and
PT infections.
XX Claim 1; Page 33-34; 75pp; English.
XX The invention relates to a cloned cDNA segment encoding a cell surface
CC antigen selected from CD1a, CD1b, CD1c, CD2, CD6, CD7, CD13, CD14, CD16,
CC CD19, CD20, CD26, CD31, CD32a, CD32b, CD33, CD34, CD36,
CC CD37, CD38, CD39, CD40, CD43 and their functional derivatives. The cell
CC surface antigens of human lymphocytes prepared from the cDNAs are useful
CC in diagnostic and therapeutic utility in immune-mediated disorders
CC (asthma, rheumatoid arthritis, multiple sclerosis, vasculitis and
CC inflammation) and infections in mammals, including humans. The present
CC sequence represents a human cell surface antigen cDNA.
XX Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;
Query Match 100.0%; Score 1200; DB 12; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGCAAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
Db 1 GGGGTGCAAGAGAGAGACAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
Qy 61 CAGCAACTGGGCACAGAAAGAGCGCGCTGGCAGGAGCACCATTGGCAGCGGCACATCCCTG 120
Db 61 CAGCAACTGGGCACAGAAAGAGCGCGCTGGCAGGAGCACCATTGGCAGCGGCACATCCCTG 120
Qy 121 GTGGCTGTGCGTTCTGGGAGCCCTGTGGTGGGCTCTCAGCTACTCCAGCCCCCAAGACTG 180
Db 121 GTGGCTGTGCGTTCTGGGAGCCCTGTGGTGGGCTCTCAGCTACTCCAGCCCCCAAGACTG 180
Qy 181 CCCAGAGAGGCACACTTGGGGCTCAGGGAAGAGCTGTGCTGCCAGATGTGAGCCAGGAAC 240
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Db 241 ATTCTCTGTGAAGACTGTGACAGCATAGAAAGCTGTGCTCAGTGTATCCTTGCATACC 300
Qy 301 GGGGGTCTCTCTTCTCTCTGACACCAACACCCGGCCCACTGTGAGAGCTGTGGCACTG 360
Db 301 GGGGGTCTCTCTTCTCTCTGACACCAACACCCGGCCCACTGTGAGAGCTGTGGCACTG 360
Qy 361 TAACTCTGCTCTTCTGTTGCGCAATGCAACCACTCACTGCAATGCTGAGTGCCTGTGCG 420
Db 361 TAACTCTGCTCTTCTGTTGCGCAATGCAACCACTCACTGCAATGCTGAGTGCCTGTGCG 420
Qy 421 CAATGGCTGGCAGTGCAGGGACAAGAGGTGCACCGAGTGTGATCCTCTTCCAAACCTTC 480
Db 421 CAATGGCTGGCAGTGCAGGGACAAGAGGTGCACCGAGTGTGATCCTCTTCCAAACCTTC 480
Qy 481 GCTGACCGCTCGGTCTCTCAGGCCCTGAGCCCAACACCCCTCAGCCCACTTACCTTA 540
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Qy 661 CGATTTTATTCGCATCCTTGTGATCTTCTTGAATGTTCTTGTGTTTTCACCTTGGCCGG 720
Db 661 CGATTTTATTCGCATCCTTGTGATCTTCTTGAATGTTCTTGTGTTTTCACCTTGGCCGG 720
Qy 721 GGCCTGTTCCTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA 780
Db 721 GGCCTGTTCCTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA 780
Qy 781 GCTGACAGGCTTGTGCTTACGCTGCCCGAGGAGGAGGCGGAGCAGACCATCCCAT 840
Db 781 GCTGACAGGCTTGTGCTTACGCTGCCCGAGGAGGAGGCGGAGCAGACCATCCCAT 840
Qy 841 CCAGGAGGATTTACCGAAACCGGAGGCTGCTCTCTCCCTCGAGCCAGCAGCCTGCGGTAG 900
Db 841 CCAGGAGGATTTACCGAAACCGGAGGCTGCTCTCTCCCTCGAGCCAGCAGCCTGCGGTAG 900
Qy 901 CTGCACTACAGCCCTGGCTTCCACCCCACTCCAGCCGCGACCATCAAGGGAGAGTGAGACC 960
Db 901 CTGCACTACAGCCCTGGCTTCCACCCCACTCCAGCCGCGACCATCAAGGGAGAGTGAGACC 960
Qy 961 TGGCAGCCCAACTGCAAGTCCCATCTCTTGTGTCAGGGCCCTTCTCTGTGTACAGTGCAC 1020
Db 961 TGGCAGCCCAACTGCAAGTCCCATCTCTTGTGTCAGGGCCCTTCTCTGTGTACAGTGCAC 1020
Qy 1021 GAGTGCCTTTTCGAGACTGGCAGGACGAGGACAAATATGATGATGAGTGGAGATGGGAA 1080
Db 1021 GAGTGCCTTTTCGAGACTGGCAGGACGAGGACAAATATGATGAGTGGAGATGGGAA 1080
Qy 1081 GCAGGAGCCCAAGCAGCTGCGCGCGTGCAGAGGGCGGGGCTCTGTGTTGTAAGGCAC 1140
Db 1081 GCAGGAGCCCAAGCAGCTGCGCGCGTGCAGAGGGCGGGGCTCTGTGTTGTAAGGCAC 1140
Qy 1141 ACTTCTGTGCGAAGAGCCCATCTGTACAGCGGCAAAATAAAGTGCAGAGTGCAC 1200
Db 1141 ACTTCTGTGCGAAGAGCCCATCTGTGTACAGCGGCAAAATAAAGTGCAGAGTGCAC 1200
RESULT 5
AAQ21183
ID AAQ21183 standard; DNA; 1203 BP.
XX
AC AAQ21183;
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1992 (first entry)
XX
XX Encodes T lymphocyte-specific CD27 Antigen.
XX Rapid immunoselection cloning technique; cell surface antigen;
XX carcinoma antigen CD40; ss.
XX Homo sapiens.
XX
```

Key	Location/Qualifiers	
sig_peptide	101..160	
mat_peptide	161..880	
	/tag= a	
	/tag= b	
PN	WO9201049-A.	
XX		
XX	23-JAN-1992.	
XX		
PF	13-JUL-1990; 90US-00553759.	
XX		
PR	13-JUL-1990; 90US-00553759.	
XX		
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
P1	Seed B, Aruffo A, Amiot M;	
XX		
XX	WPI; 1992-056864/07.	
DR	P-PSDB; AAR20814.	
XX		
XX	New CD53 cell surface antigen and DNA encoding it - for immuno-therapy	
PT	and diagnosis of haematopoietic neoplasms, etc.	
PT		
XX		
PS	Example 13; Page 103; 160pp; English.	
XX		
CC	A cDNA clone encoding CD27 was obtained from human T lymphocyte cDNA	
CC	transferred into COS cells and immunoselected using the Mabs OKT18a and	
CC	CLB-9f4 (see e.g. AAO1164 for description of the rapid immunoselection	
CC	cloning method). A positive vector contained a 1.2kb insert. The ability	
CC	to interfere with the binding of CD27 positive T cells with antigen	
CC	presenting cells, or the ability to cause such binding to occur on	
CC	surfaces other than lymphocyte cells, can be useful in diagnostics and	
CC	therapy. (Updated on 25-MAR-2003 to correct FA field.)	
XX		
SQ	Sequence 1203 BP; 261 A; 375 C; 341 G; 226 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1200; DB 2; Length 1203;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GGGGTGCAAGAGACAGACAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60	
DB	1 GGGGTGCAAGAGAGACAGACAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60	
QY	61 CAGCAACTGGGCACAGAAAGAGCGCGCTGGGAGGGACCATGGCACGGCCATCCCTG 120	
DB	61 CAGCAACTGGGCACAGAAAGAGCGCGCTGGGAGGGACCATGGCACGGCCATCCCTG 120	
QY	121 GTGGCTGTGCTTCTGGGACCGCTGTGGGCTCTCAGCTACTCCAGGCCCCCAAGAGCTG 180	
DB	121 GTGGCTGTGCTTCTGGGACCGCTGTGGGCTCTCAGCTACTCCAGGCCCCCAAGAGCTG 180	
QY	181 CCAGAGAGGCACACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240	
DB	181 CCAGAGAGGCACACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240	
QY	241 ATTCTCTGTGAAGGACTGTGACACAGCATAGAAAGGCTGTCTAGTGTGATCCTTGGATACC 300	
DB	241 ATTCTCTGTGAAGGACTGTGACACAGCATAGAAAGGCTGTCTAGTGTGATCCTTGGATACC 300	
QY	301 GGGGGTCTCTTCTCTCTGACCAACACACCGGCCCTCTGTGAGAGCTGTGGCAGCTG 360	
DB	301 GGGGGTCTCTTCTCTCTGACCAACACACCGGCCCTCTGTGAGAGCTGTGGCAGCTG 360	
QY	361 TAACTCTGGTCTTCTCTGTTGGCAACTGCACCATCACTGCCAATGTGAGTGTGCTGTGCG 420	
DB	361 TAACTCTGGTCTTCTCTGTTGGCAACTGCACCATCACTGCCAATGTGAGTGTGCTGTGCG 420	
QY	421 CAATGCTGGCAGTGACGGACAAGAGGTGACCGAGTGTGATCCTTCTCCAAACCCCTTC 480	
DB	421 CAATGCTGGCAGTGACGGACAAGAGGTGACCGAGTGTGATCCTTCTCCAAACCCCTTC 480	

QY	481	GTGTACCCGCTCGGTGGTGTCTCAGGCCCTGAGCCACACACCTCAGCCACCACCTTACTCTTA	540
DB	481	GTGTACCCGCTCGGTGGTGTCTCAGGCCCTGAGCCACACACCTCAGCCACCACCTTACTCTTA	540
QY	541	TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCAATGCGACATCTGGCTGACTTCAG	600
DB	541	TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCAATGCGACATCTGGCTGACTTCAG	600
QY	601	GCAGCTGCTGCCCGGAGCTCTCTACCCACCTGGGCCACCCCAAGATCCTGTGCGACTC	660
DB	601	GCAGCTGCTGCCCGGAGCTCTCTACCCACCTGGGCCACCCCAAGATCCTGTGCGACTC	660
QY	661	CGATTTTATTGCGATCCTTGTGATCTTCTCGAATGTTCTTGTGTTTCACTCCCTGGCCGG	720
DB	661	CGATTTTATTGCGATCCTTGTGATCTTCTCGAATGTTCTTGTGTTTCACTCCCTGGCCGG	720
QY	721	GGCCCTGTTTCTCCATCAACGAAGGAAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA	780
DB	721	GGCCCTGTTTCTCCATCAACGAAGGAAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA	780
QY	781	GCCTGACAGCTTGTGCTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
DB	781	GCCTGACAGCTTGTGCTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
QY	841	CCAGGAGGATTACCGAAACCGGAGCTGCTGCTCCCTGAGCCAGCCAGCAGCAGCTGCGGTAG	900
DB	841	CCAGGAGGATTACCGAAACCGGAGCTGCTGCTCCCTGAGCCAGCCAGCAGCAGCTGCGGTAG	900
QY	901	CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGCGGACCATCCAAAGGAGAGTGAGACC	960
DB	901	CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGCGGACCATCCAAAGGAGAGTGAGACC	960
QY	961	TGGCAGCCACAACCTGAGTCCCATCTCTTGTGAGGGCCCTTCTCTGTGTACACGTGACA	1020
DB	961	TGGCAGCCACAACCTGAGTCCCATCTCTTGTGAGGGCCCTTCTCTGTGTACACGTGACA	1020
QY	1021	GAGTGCCTTTTCGAGACTGGCAGGACGAGGACAAATATGAGTGTGAGGTGGAGTGGGAA	1080
DB	1021	GAGTGCCTTTTCGAGACTGGCAGGACGAGGACAAATATGAGTGTGAGGTGGAGTGGGAA	1080
QY	1081	GCAGAGGCCACGCCAGCTGCGCGCGTGCAGAGGGGGGGGCTCTGTTGTTAAGGCAC	1140
DB	1081	GCAGAGGCCACGCCAGCTGCGCGCGTGCAGAGGGGGGGGCTCTGTTGTTAAGGCAC	1140
QY	1141	ACTTCTGCTGCGAAGACCCACATGCTACAGACGGGCAAAATTAAGTGCAGATGACC	1200
DB	1141	ACTTCTGCTGCGAAGACCCACATGCTACAGACGGGCAAAATTAAGTGCAGATGACC	1200

RESULT 6

AAT14722

ID AAT14722 standard; cDNA; 1200 BP.

XX AAT14722;

AC AC

XX 25-MAR-2003 (revised)

DT 31-OCT-1996 (first entry)

XX Human CD27 antigen cDNA.

XX Cell surface antigen; cloning; immunoselection; immunotherapy; therapy;

KW diagnosis; vector; COS; CD27; T-lymphocyte; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 101..883

FT /tag= a

FT /transl_except= (200..202, aa:Arg)

FT /transl_except= (413..415, aa:Ala)

FT sig_peptide 101..160

FT /tag= b

FT mat_peptide 161..880


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FT FT misc_difference /*tag= c
FT FT 742 /tag= d
FT FT /note= "an additional adenine base at position 742 is
FT FT given in the specification, but interrupts the reading
FT FT frame"
XX XX US5506126-A.
XX XX
XX XX 09-APR-1996.
XX XX
XX XX 18-OCT-1993; 93US-00139273.
XX XX
XX XX 25-FEB-1988; 88US-00160416.
XX XX 13-JUL-1989; 89US-00379076.
XX XX 13-JUL-1990; 90US-00553759.
XX XX 01-DEC-1992; 92US-00983647.
XX XX
XX XX (GEO ) GEN HOSPITAL CORP.
XX XX
XX XX Seed B, Aruffo A;
XX XX
XX XX WPI; 1996-200279/20.
XX XX P-PSDB; AAR91441.
XX XX
XX XX Cloning of cDNA encoding cell surface antigen - useful for isolation of
XX XX diagnostic and therapeutic proteins.
XX XX
XX XX Example 13; Col 67-68; 79pp; English.
XX XX
XX XX A cDNA clone (AAT14722) codes for human antigen CD27 (AAR91441), a T-
XX XX lymphocyte activation antigen. It was obtd. by constructing an expression
XX XX library in COS cells using T-lymphocyte cDNA, and immunoselecting with
XX XX monoclonal antibodies OKT18a and CLB-9F4. This immunoselection cloning
XX XX method, developed to clone genes for cell surface antigens of human
XX XX lymphocytes (see also AAT14703-04 and AAT14706-26), has general appln.
XX XX Cell surface antigens are obtd. for diagnostic and therapeutic use.
XX XX (Updated on 25-MAR-2003 to correct PF field.)
XX XX
XX XX Sequence 1200 BP; 259 A; 372 C; 342 G; 227 T; 0 U; 0 Other;
XX XX
XX XX Query Match 99.7%; Score 1196.8; DB 2; Length 1200;
XX XX Best Local Similarity 99.8%; Pred. No. 0;
XX XX Matches 1198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGTGCNAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGCCAGCAT 60
DB 1 GGGGTGCNAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGCCAGCAT 60
QY 61 CAGCACTGGGCACAGAAAGAGCGCGCTGGCGAGGACCATGGCACGGCCACATCCCTG 120
DB 61 CAGCACTGGGCACAGAAAGAGCGCGCTGGCGAGGACCATGGCACGGCCACATCCCTG 120
QY 121 GTGGCTGTGCGTTCTGGGGAACCTGTGGGTCTCTAGCTACTCCAGCCCCCAAGAGCTG 180
DB 121 GTGGCTGTGCGTTCTGGGGAACCTGTGGGTCTCTAGCTACTCCAGCCCCCAAGAGCTG 180
QY 181 CCAGAGAGGCACTACTGGGCTCAGGGAAGAGCTGTGCTGCCAGATGTGTAGCCAGGAAC 240
DB 181 CCAGAGAGGCACTACTGGGCTCAGGGAAGAGCTGTGCTGCCAGATGTGTAGCCAGGAAC 240
QY 241 ATTCTCTGTGAGGACGTGACAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
DB 241 ATTCTCTGTGAGGACGTGACAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
QY 301 GGGGGTCTCTCTCTCTGACACCAACACCGGCGCCCACTGTGAGAGCTGTGGCACTG 360
DB 301 GGGGGTCTCTCTCTCTGACACCAACACCGGCGCCCACTGTGAGAGCTGTGGCACTG 360
QY 361 TAACTCTGGTCTTCTGTTGGCAACTGACCATCACTGCCAATGCTGAGTGTGCTGTG 420
DB 361 TAACTCTGGTCTTCTGTTGGCAACTGACCATCACTGCCAATGCTGAGTGTGCTGTG 420

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QY 421 CAATGCTGGAGTGCAGGGACAAAGAGTGCACCGAGTGTGATCCTCTTCCAAACCTTTC 480
DB 421 CAATGCTGGAGTGCAGGGACAAAGAGTGCACCGAGTGTGATCCTCTTCCAAACCTTTC 480
QY 481 GCTGACCGCTCGGTGCTCTCAGGCCCTGAGCCACACACCTCAGCCACACCCACTTACCTTA 540
DB 481 GCTGACCGCTCGGTGCTCTCAGGCCCTGAGCCACACACCTCAGCCACACCCACTTACCTTA 540
QY 541 TGTCACTGAGATGCTGGAGGCCAGGACAGCTGGGCAATGCAAGTCTTGCTGACTTTCAG 600
DB 541 TGTCACTGAGATGCTGGAGGCCAGGACAGCTGGGCAATGCAAGTCTTGCTGACTTTCAG 600
QY 601 GCAGTGCCTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGCAGCTC 660
DB 601 GCAGTGCCTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGCAGCTC 660
QY 661 CGATTTTATTGTCATCCTTGTGATCTTCTGGAATGTTCTTGTGTTTCACTTGGCCGG 720
DB 661 CGATTTTATTGTCATCCTTGTGATCTTCTGGAATGTTCTTGTGTTTCACTTGGCCGG 720
QY 721 GGCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
DB 721 GGCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGTGA 780
QY 781 GCTGCAGAGCCTTGTGTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCTGCAGAGCCTTGTGTTACAGCTGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 CCAGGAGGATTAACCGAAACCGGAGCCTGCCTGCCCTCCCTGAGCCAGCACCTGCGGTAG 900
DB 841 CCAGGAGGATTAACCGAAACCGGAGCCTGCCTGCCCTCCCTGAGCCAGCACCTGCGGTAG 900
QY 901 CTGCACTACAGCCCTGGCTCCACCCCGGACCCCGGACCATCCAAAGGAGAGTGTGAGACC 960
DB 901 CTGCACTACAGCCCTGGCTCCACCCCGGACCCCGGACCATCCAAAGGAGAGTGTGAGACC 960
QY 961 TGGACGCCCAACTGCACTGCCATCTCTTGTGTCAGGGCCCTTTCCTGTGTACAGTGACA 1020
DB 961 TGGACGCCCAACTGCACTGCCATCTCTTGTGTCAGGGCCCTTTCCTGTGTACAGTGACA 1020
QY 1021 GAGTGCCTTTTCGAGACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 GAGTGCCTTTTCGAGACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GCAGAGGCCAGCAGCAGCTGCGCGCTGTCAGAGGCGCGGGGCTCTGTGTTGTAAGGCAC 1140
DB 1081 GCAGAGGCCAGCAGCAGCTGCGCGCTGTCAGAGGCGCGGGGCTCTGTGTTGTAAGGCAC 1140
QY 1141 ACTTCTGTGCGAAAGACCCATGCTACAAGACGGGGCAAAATAAAGTGACAGATGACC 1200
DB 1141 ACTTCTGTGCGAAAGACCCATGCTACAAGACGGGGCAAAATAAAGTGACAGATGACC 1200

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RESULT 7
AAA50595
ID AAA50595 standard; cDNA; 1200 BP.
XX
AC AAA50595;
XX
DT 19-DEC-2000 (first entry)
XX
DE Human cell surface antigen CD27 cDNA.
XX
KW CD27; cell surface antigen; human; immunoselection; panning;
KW immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune disorder;
KW infection; asthma; immune-complex disease; amyloidosis;
KW multiple sclerosis; parasitic disease; autoimmune disease; T-lymphocyte;
KW ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 101..883
FT

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FT      /*tag= a
FT      /transl_except= (pos:200. .202, aa:Arg)
FT      sig_peptide
FT      101..160
FT      /*tag= b
FT      mat_peptide
FT      161..880
FT      /*tag= c
PN      US6111093-A.
XX      29-AUG-2000.
XX      28-OCT-1998; 98US-00181612.
XX      25-FEB-1988; 88US-00160416.
XX      13-JUL-1989; 89US-00379076.
XX      23-MAR-1990; 90US-00498809.
XX      13-JUL-1990; 90US-00553759.
XX      01-DEC-1992; 92US-00983647.
XX      (GEO ) GEN HOSPITAL CORP.
XX      Stamenkovic I, Seed B;
XX      WPI; 2000-586382/55.
XX      P-PSDB; AAY96137.
XX      Isolated nucleic acid molecule encoding the CD19 cell surface antigen,
XX      useful for immunodiagnosis and immunotherapy of immune-mediated
XX      infections or disorders, e.g. asthma, immune-complex disease, parasitic
XX      diseases.
XX      Example 13; Col 67-68; 75pp; English.
XX      The present sequence is that of cDNA encoding human cell surface antigen
XX      (CSA) CD27 (see AAY96137), a T-lymphocyte activation antigen. The cDNA
XX      was isolated from a human T-lymphocyte cDNA introduced into COS cells and
XX      screened using a novel method of the invention. The method, designed to
XX      isolate CSA nucleic acids, is based upon transient expression of a CSA in
XX      eukaryotic cells and physical selection of cells expressing the antigen
XX      by adhesion to (panning on) an antibody-coated substrate such as a
XX      culture dish. CSA nucleic acids isolated by the method of the invention,
XX      and the proteins they encode, are useful for immunodiagnostic and
XX      immunotherapeutic applications, including the diagnosis and treatment of
XX      immune-mediated infections, diseases, and disorders in animals, including
XX      humans. These disorders include aschma, immune-complex disease,
XX      amyloidosis, parasitic diseases or multiple sclerosis. The ability to
XX      interfere with the binding of CD27 positive T cells with antigen
XX      presenting cells, or the ability to cause such binding to occur on
XX      surfaces other than lymphocyte cells, can be useful in diagnostics and
XX      therapy. A soluble CD27 fusion protein will be useful to prevent
XX      undesired T cell proliferation in certain autoimmune diseases
XX      SQ      Sequence 1200 BP; 260 A; 371 C; 343 G; 226 T; 0 U; 0 Other;
XX      Query Match          99.7%; Score 1196.8; DB 3; Length 1200;
XX      Best Local Similarity 99.8%; Pred.No. 0; Mismatches 0; Gaps 0;
XX      Matches 1198; Conservative 0; Indels 2; Indels 0; Gaps 0;
XX      QY      1 GGGGTGCAAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
XX      DB      1 GGGGTGCAAGAGAGACAGACGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
XX      QY      61 CAGCAACTGGGCACAGAAAGAGAGCCCGCTGGGAGGACCATGGCAAGGCCACATCCCTG 120
XX      DB      61 CAGCAACTGGGCACAGAAAGAGAGCCCGCTGGGAGGAGATGGCAAGGCCACATCCCTG 120
XX      QY      121 GTGGCTGTGGCTTCTGGGACCCCTGGTGGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180
XX      DB      121 GTGGCTGTGGCTTCTGGGACCCCTGGTGGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180
XX      QY      181 CCCAGAGAGGCACTACTTGGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
XX      DB      181 CCCAGAGAGGCACTACTTGGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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QY      241 ATTCCTCGTAGGAGCTGTGACCAAGAGAGCTGCTCAGTGTGATCCTTGCATACC 300
DB      241 ATTCCTCGTAGGAGCTGTGACCAAGAGAGCTGCTCAGTGTGATCCTTGCATACC 300
QY      301 GGGGGTCTCCTTCTCTCTGACACACACCGCGGCCCACTGTGAGAGCTGTGCGGACTG 360
DB      301 GGGGGTCTCCTTCTCTCTGACACACACCGCGGCCCACTGTGAGAGCTGTGCGGACTG 360
QY      361 TAACTCTGGTCTTCTGCTTGGCAAATGCAACCATCACTGCAATGTGTGCTGTGCTG 420
DB      361 TAACTCTGGTCTTCTGCTTGGCAAATGCAACCATCACTGCAATGTGTGCTGTGCTG 420
QY      421 CAAATGGCTGGCAGTGCAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCCTTC 480
DB      421 CAAATGGCTGGCAGTGCAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCCTTC 480
QY      481 GCTGACCGCTCGGTCTCTCAGGCCCTGAGCCCAACACCTCAGCCCACTTACTTTA 540
DB      481 GCTGACCGCTCGGTCTCTCAGGCCCTGAGCCCAACACCTCAGCCCACTTACTTTA 540
QY      541 TGTCAGTGAGATGTCTGGAGGCGAGACAGCTGGGCAATGCAAGTCTTGGCTGACTTCAG 600
DB      541 TGTCAGTGAGATGTCTGGAGGCGAGACAGCTGGGCAATGCAAGTCTTGGCTGACTTCAG 600
QY      601 GCAGCTGCTGCCCGGACTCTCTACCACTGGGCCACCCCAAGATCCTGTGCACTC 660
DB      601 GCAGCTGCTGCCCGGACTCTCTACCACTGGGCCACCCCAAGATCCTGTGCACTC 660
QY      661 CGATTTTATTCGCATCTTGTGATCTTCTCTGGAATGTTCTTGTGTTTCACTTGGCCGG 720
DB      661 CGATTTTATTCGCATCTTGTGATCTTCTCTGGAATGTTCTTGTGTTTCACTTGGCCGG 720
QY      721 GGCCTGTCTCTCCATCAACGAAGAAATATAGATCAAAAGAGAGAAAGTCTGTGGA 780
DB      721 GGCCTGTCTCTCCATCAACGAAGAAATATAGATCAAAAGAGAGAAAGTCTGTGGA 780
QY      781 GCCTCAGAGCTTCTGTTACAGCTGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB      781 GCCTCAGAGCTTCTGTTACAGCTGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY      841 CCAGAGAGATTAACCAAAACCGGAGCTGCTCTCCCTCGAGCCAGCACCTGCGGTAG 900
DB      841 CCAGAGAGATTAACCAAAACCGGAGCTGCTCTCCCTCGAGCCAGCACCTGCGGTAG 900
QY      901 CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGCGACCATCCAAAGGAGAGTGAGACC 960
DB      901 CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGCGACCATCCAAAGGAGAGTGAGACC 960
QY      961 TGGGAGCCCACTGCACTGCTTGTGTCAGGGCCCTTCTCTGTGTCACAGTGACA 1020
DB      961 TGGGAGCCCACTGCACTGCTTGTGTCAGGGCCCTTCTCTGTGTCACAGTGACA 1020
QY      1021 GAGTGCCTTTTCGAGACTGGCAGGAGCAGAGGACAAATATGAGATGAGGTGGAGTGGGAA 1080
DB      1021 GAGTGCCTTTTCGAGACTGGCAGGAGCAGAGGACAAATATGAGATGAGGTGGAGTGGGAA 1080
QY      1081 GCAGGAGCCAGCCAGCTGCGCGCTGCAAGAGGCGGGGGCTCTGTTGTAAGGCAC 1140
DB      1081 GCAGGAGCCAGCCAGCTGCGCGCTGCAAGAGGCGGGGGCTCTGTTGTAAGGCAC 1140
QY      1141 ACTTCTGCTGCAAGAGCCCACTGCTTACAGAGCGGGCAAAATAAAGTGCAGATGACC 1200
DB      1141 ACTTCTGCTGCAAGAGCCCACTGCTTACAGAGCGGGCAAAATAAAGTGCAGATGACC 1200
XX      RESULT 8
XX      ID ABQ80112 standard; cDNA; 1204 BP.
XX      AC ABQ80112;
XX      DT 13-JUN-2003 (first entry)
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RESULT 9	
ACA64893	
ID ACA64893 standard; DNA; 1204 BP.	
XX AC ACA64893;	
XX 27-JUN-2003 (first entry)	
XX Human CD27 DNA corresponding to M63928.	
XX Human; chronic inflammatory joint disease; infection; tumour;	
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;	
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.	
OS Homo sapiens.	
XX DE10127572-A1.	
XX 05-DEC-2002.	
XX 30-MAY-2001; 2001DE-01027572.	
XX 30-MAY-2001; 2001DE-01027572.	
XX (PATH-) PATHOARRAY GMBH.	
XX Haupl T, Ungethuen U, Blaess S;	
XX WPI; 2003-240797/24.	
XX Reagents for diagnosis, study and therapy of chronic inflammatory joint	
PT and other diseases, comprises any of many specified genes or derived	
PT proteins.	
XX Claim 1; Page; 12pp; German.	
XX This invention describes a novel reagent for diagnosis, molecular	
CC definition and therapy of chronic inflammatory joint diseases, and other	
CC inflammatory disorders, infective or tumour diseases in humans. The	
CC products of the invention have antiinflammatory, cytostatic,	
CC antiarthritic, antirheumatic and immunosuppressive activity, and can be	
CC used for gene therapy. The reagent of the invention and any proteins and	
CC antibodies derived from it, are used (i) for analysing tissue and blood	
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of	
CC chronic joint diseases, on the basis of molecular characterisation, and	
CC determining the etiological pathogenicity principle of as yet	
CC uncharacterised inflammatory diseases, also monitoring progression and/or	
CC treatment of disease, and optimisation of therapy and (iii) for	
CC developing treatments for inflammatory diseases, particularly of joints,	
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides	
CC used in the method of the invention	
XX Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;	
XX Query Match 98.5%; Score 1182.6; DB 8; Length 1204;	
XX Best Local Similarity 99.6%; Pred. No. 0;	
XX Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;	
QY 1 GGGGTGCAAGAGAGACAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60	
DB 1 GGGGTGCAAGAGAGACAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60	
QY 61 CAGCAACTGGGCACAGAAAGAGGCCCGCTGGGAGGGACCATGGACGGCCACATCCCTG 120	
DB 61 CAGCAACTGGGCACAGAAAGAGGCCCGCTGGGAGGGACCATGGACGGCCACATCCCTG 120	
QY 121 GTGGCTGTGGTCTCGGGACCCCTGTGGGGCTCTCAGCTACTCCAGGCCCCCAAGAGCTG 180	
DB 121 GTGGCTGTGGTCTCGGGACCCCTGTGGGGCTCTCAGCTACTCCAGGCCCCCAAGAGCTG 180	
QY 181 CCCAGAGAGGCACACTCTGGGGCTCAGGGAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240	
DB 181 CCCAGAGAGGCACACTCTGGGGCTCAGGGAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240	

Db	181	CCCAGAGAGGCACACTCTGGGGCTCAGGGAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC	240
Qy	241	ATTCTCTCGTGAAGGACTGTGACACCATAGAAGGCTGCTCAGTGTGATCCTTGCATACC	300
Db	241	ATTCTCTCGTGAAGGACTGTGACACCATAGAAGGCTGCTCAGTGTGATCCTTGCATACC	300
Qy	301	GGGGGTCTCTCTCTCTCTGACACACACCCGGGCCCACTGTGAGAGCTGTGCGGACTG	360
Db	301	GGGGGTCTCTCTCTCTCTGACACACACCCGGGCCCACTGTGAGAGCTGTGCGGACTG	360
Qy	361	TAACTCTGCTCTCTCTCTGCAACTGCAACATCACTGCAATGTGAGTGTGCTGTGCG	420
Db	361	TAACTCTGCTCTCTCTCTGCAACTGCAACATCACTGCAATGTGAGTGTGCTGTGCG	420
Qy	421	CAATGGCTGGCAGTGCAGGGACAAAGAGTGCACCGAGTGTGATCTCTTCCAAACCTTC	480
Db	421	CAATGGCTGGCAGTGCAGGGACAAAGAGTGTGATCTCTTCCAAACCTTC	480
Qy	481	GCTGACCGCTCGGTCTCTCAGGCCCTGAGGCCACACCCCTCAGCCCAACCACTTACTTA	540
Db	481	GCTGACCGCTCGGTCTCTCAGGCCCTGAGGCCACACCCCTCAGCCCAACCACTTACTTA	540
Qy	541	TCTCAGTGTGATGTCTGGAGGCCAGACAGCTGGGCACATGCAAGCTCTGGCTGACTGAG	600
Db	541	TCTCAGTGTGATGTCTGGAGGCCAGACAGCTGGGCACATGCAAGCTCTGGCTGACTGAG	600
Qy	601	GCAGCTGGCTGGCCGGACTCTCTTACCCACTGGGCACCCCAAGATCCTCTGCAAGCTC	660
Db	601	GCAGCTGGCTGGCCGGACTCTCTTACCCACTGGGCACCCCAAGATCCTCTGCAAGCTC	660
Qy	661	CGATTTTATTCATCTCTTGTGATCTTCTCTGGAATGTTCTTGTTCACCTGCGCCGG	720
Db	661	CGATTTTATTCATCTCTTGTGATCTTCTCTGGAATGTTCTTGTTCACCTGCGCCGG	720
Qy	721	GGCCCTGTTCTCCATCAACGAAGAAATATAGATCAAAACGAAGGAAGTCTCTGTGA	780
Db	721	GGCCCTGTTCTCCATCAACGAAGAAATATAGATCAAAACGAAGGAAGTCTCTGTGA	780
Qy	781	GCCTCAGAGCCTTCTCGTTACAGCTGCCCGAGGAGGAGGCGCAGCACCATCCCCAT	840
Db	781	GCCTCAGAGCCTTCTCGTTACAGCTGCCCGAGGAGGAGGCGCAGCACCATCCCCAT	840
Qy	841	CCAGGAGGATTAACCGAAACCCGAGCTGCTCTCCCTCGAGCCAGCACCTGCGGTAG	900
Db	841	CCAGGAGGATTAACCGAAACCCGAGCTGCTCTCCCTCGAGCCAGCACCTGCGGTAG	900
Qy	901	CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGGACCATCCAAAGGAGAGTGAGACC	960
Db	901	CTGCACTACAGCCCTGGGCTCCACCCCAACCCCGGACCATCCAAAGGAGAGTGAGACC	960
Qy	961	TGGCAGCCACAACCTGCAGTCCCATCTCTTGTTCAGGGGCCCTTCTCTGTACACGTGAC	1020
Db	961	TGGCAGCCACAACCTGCAGTCCCATCTCTTGTTCAGGGGCCCTTCTCTGTACACGTGAC	1020
Qy	1021	GAGTGCCCTTTTCGAGACTGGCAGGACAGGACAAATATGGATGAGGTGGAGTGGGAA	1080
Db	1021	GAGTGCCCTTTTCGAGACTGGCAGGACAGGACAAATATGGATGAGGTGGAGTGGGAA	1080
Qy	1081	GCAGGAGCCAGCAGCTGCGGCTGCGCTGAGGAGGGCGGGGCTCTGGTTGTAAGGCA	1139
Db	1081	GCAGGAGCCAGCAGCTGCGGCTGCGCTGAGGAGGGCGGGGCTCTGGTTGTAAGGCA	1140
Qy	1140	CACTTCTGCTGCGAAAGACCCACATGCTACAAAGAGGGCAAAATTAAGTGCAGATGAC	1199
Db	1141	CACTTCTGCTGCGAAAGACCCACATGCTACAAAGAGGGCAAAATTAAGTGCAGATGAC	1199
Qy	1200	C 1200	
Db	1201	C 1201	

RESULT 10
ADD25535

XX Homo sapiens.
OS WO2003068268-A2.
PN
XX
XX 21-AUG-2003.
PD
XX 13-FEB-2003; 2003WO-BP001461.
PF
XX 14-FEB-2002; 2002GB-00003480.
PR 29-JUN-2002; 2002GB-00015095.
XX
XX (BIOI-) BIOINVENT INT AB.
PA
XX
XX Ek S, Borrebaeck CAK, Ehinger M;
PI WPI; 2003-697496/66.
XX P-PSDB; ADL15013.
DR
XX
XX New compound for treating, imaging, diagnosing or prognosing mantle cell
PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT protein (e.g. human autotoxin polypeptide), and a further moiety (e.g.
PT nucleic acid).
PT
XX
XX Disclosure; SEQ ID NO 26; 342pp; English.
PS
XX
XX The invention relates to a compound comprising a binding moiety which
CC selectively binds to a protein or polypeptide listed in the specification
CC (e.g. human autotoxin polypeptide or human CD24 signal transducer
CC polypeptide), and a further moiety. The compound is useful in medicine or
CC in the treatment, imaging, diagnosis or prognosis of mantle cell
CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC in the body of an individual. This sequence corresponds to a gene
CC encoding one of the polypeptides of the invention.
XX
XX Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;
SQ

Query Match 98.5%; Score 1182.6; DB 10; Length 1204;
Best Local Similarity 99.6%; Pred. NO. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GGGGTCAAGAGACAGACAGCGCCAGCTTGGAGTGCTAACTCCAGAGGCCAGCAT 60
DB 1 GGGGTCAAGAGAGACAGACAGCGCCAGCTTGGAGTGCTAACTCCAGAGGCCAGCAT 60

QY 61 CAGCAACTGGGCACAGAAAGAGCGCCCTGGGCAGGACCATGGCAGGCCACATCCCTG 120
DB 61 CAGCAACTGGGCACAGAAAGAGCGCCCTGGGCAGGACCATGGCAGGCCACATCCCTG 120

QY 121 GTGGCTGTGCTGTGGGACCGCTGTGGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180
DB 121 GTGGCTGTGCTGTGGGACCGCTGTGGGGCTCTCAGTACTCCAGCCCCCAAGAGCTG 180

QY 181 CCAGAGAGCGCACTACTGGGCTCAGGAAAGCTGTGCTCCAGATGTGTGAGCCAGGAAC 240
DB 181 CCAGAGAGCGCACTACTGGGCTCAGGAAAGCTGTGCTCCAGATGTGTGAGCCAGGAAC 240

QY 241 ATTCTCTGTGAAGGACTGTGACAGCATAGAAGGCTGTGCTGATGCTTGTGATACC 300
DB 241 ATTCTCTGTGAAGGACTGTGACAGCATAGAAGGCTGTGCTGATGCTTGTGATACC 300

QY 301 GGGGCTCTCTCTCTCTCTGACCAACACCCGGGCCCACTGTGTGAGAGCTGTGGGACTG 360
DB 301 GGGGCTCTCTCTCTCTCTGACCAACACCCGGGCCCACTGTGTGAGAGCTGTGGGACTG 360

QY 361 TAACTCTGTCTCTCTCTCTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCTG 420
DB 361 TAACTCTGTCTCTCTCTCTGCTGCACTGCACTGCACTGCACTGCACTGCTGCTG 420

QY 421 CAATGGCTGGCAGTGACAGGACCAAGAGGTGACCGAGTGATCTCTTCCAAACCCCTTC 480
DB 421 CAATGGCTGGCAGTGACAGGACCAAGAGGTGACCGAGTGATCTCTTCCAAACCCCTTC 480

QY 481 GCTGACCGCTGGTCTCTCAGGCGCTTGAGCCACACCTCTCAGCCACCCACTTACCTTA 540
DB 481 GCTGACCGCTGGTCTCTCAGGCGCTTGAGCCACACCTCTCAGCCACCCACTTACCTTA 540

QY 541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGACAGACTCTGGCTGACTTCAG 600
DB 541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGACAGACTCTGGCTGACTTCAG 600

QY 601 GCAGCTGCTGCCCGGACTCTCTTACCACTTGGGCACCCCAAGATCCCTGTGAGCTC 660
DB 601 GCAGCTGCTGCCCGGACTCTCTTACCACTTGGGCACCCCAAGATCCCTGTGAGCTC 660

QY 661 CGATTTTATTCGATCCTTGTGATCTCTCTGGAATGTTCTTGTGTTTTCACCTGSCCGG 720
DB 661 CGATTTTATTCGATCCTTGTGATCTCTCTGGAATGTTCTTGTGTTTTCACCTGSCCGG 720

QY 721 GGCCCTGTTCTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA 780
DB 721 GGCCCTGTTCTCCATCAACGAAGGAATATAGATCAAAACAAAGGAGAAAGTCTGTGGA 780

QY 781 GCCTCAGAGCCTTGTGTTACAGCTGCCCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCCTCAGAGCCTTGTGTTACAGCTGCCCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 840

QY 841 CCAGGAGGATTAACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 CCAGGAGGATTAACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900

QY 901 CTGCACTACAGCCCTGGGCTTCCACCCCAACCCCGCCGACCATCCCAAGGAGAGTGAGACC 960
DB 901 CTGCACTACAGCCCTGGGCTTCCACCCCAACCCCGCCGACCATCCCAAGGAGAGTGAGACC 960

QY 961 TGGCAGCCACAACTGCAGTCCCATCTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 961 TGGCAGCCACAACTGCAGTCCCATCTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020

QY 1021 GAGTCCCTTTTCGAGACTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 GAGTCCCTTTTCGAGACTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080

QY 1081 GCAGGAGCCAGCAGCTGCGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139
DB 1081 GCAGGAGCCAGCAGCTGCGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140

QY 1140 CACTTCTGTGCGAAAGACCCACATGCTTAAAGACGGGCAAAATATAAGTGACAGATGAC 1199
DB 1141 CACTTCTGTGCGAAAGACCCACATGCTTAAAGACGGGCAAAATATAAGTGACAGATGAC 1200

QY 1200 C 1200
DB 1201 C 1201

RESULT 12
ADI31701
ID ADI31701 standard; cDNA; 1204 BP.
XX
AC ADI31701;
XX AC
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #1027.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiaesthetic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.

KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
XX osteoporosis; pancreatitis; infection; arthritis; lymph node.
OS Homo sapiens.
XX US2004077003-A1.
XX 22-APR-2004.
XX 14-AUG-2003; 2003US-00641643.
XX 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2004-387937/36.
XX New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX Claim 15; SEQ ID NO 1027; 16pp; English.
XX The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

Query Match 98.5%; Score 1182.6; DB 13; Length 1204;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GGGGTGCAAGAGAGACAGCAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
DB 1 GGGGTGCAAGAGAGAGACAGCAGCGCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
QY 61 CAGCACTGGGCACAGAAAGAGCGCCCTGGCAGGACCCTAGCTACTCCAGCGGCCATCCCTG 120
DB 61 CAGCACTGGGCACAGAAAGAGCGCCCTGGCAGGACCCTAGCTACTCCAGCGGCCATCCCTG 120
QY 121 GTGGCTGTGGTCTGGGGACCTGTGGGGCTCTCAGTACTCCAGCGGCCATCCCTG 180
DB 121 GTGGCTGTGGTCTGGGGACCTGTGGGGCTCTCAGTACTCCAGCGGCCATCCCTG 180
QY 181 CCCAGAGAGGCACCTACTGGGCTCAGGGAAGCTGTGTGTCAGATGTGTGAGCCAGGAAC 240
DB 181 CCCAGAGAGGCACCTACTGGGCTCAGGGAAGCTGTGTGTCAGATGTGTGAGCCAGGAAC 240
QY 241 ATTCTCTGTGAGGACTGTGACCGAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
DB 241 ATTCTCTGTGAGGACTGTGACCGAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
QY 301 GGGGGTCTCTCTCTCTGACCAACACACCGGCCCTCTGTGAGAGCTGTGGCACTG 360
DB 301 GGGGGTCTCTCTCTCTGACCAACACACCGGCCCTCTGTGAGAGCTGTGGCACTG 360
QY 361 TAACTCTGGTCTTCTCTCGCTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTCG 420
DB 361 TAACTCTGGTCTTCTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTCG 420

QY 421 CAATGGCTGGCAGTGCAGGGACAAGAGTGCACCGAGTGTATCTCTTCCAAACCCCTTC 480
DB 421 CAATGGCTGGCAGTGCAGGGACAAGAGTGCACCGAGTGTATCTCTTCCAAACCCCTTC 480
QY 481 GCTGACCGCTCGGTGTCTCAGGCCCTGAGCCACACCTCTGAGCCACCCCTTACCTTA 540
DB 481 GCTGACCGCTCGGTGTCTCAGGCCCTGAGCCACACCTCTGAGCCACCCCTTACCTTA 540
QY 541 TGTTCAGTGTGATGTCTGAGGCCAGAGCTGGGCACATGACAGCTCTGGCTGACTTCAG 600
DB 541 TGTTCAGTGTGATGTCTGAGGCCAGAGCTGGGCACATGACAGCTCTGGCTGACTTCAG 600
QY 601 GCAGCTGCTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGAGCTC 660
DB 601 GCAGCTGCTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGAGCTC 660
QY 661 CGATTTTATTCGATCTTGTGATCTTCTCTGGAATGTTCTTGTTCACCCCTGGCCGG 720
DB 661 CGATTTTATTCGATCTTGTGATCTTCTCTGGAATGTTCTTGTTCACCCCTGGCCGG 720
QY 721 GGCCTGTTCTCCATCAACGAGGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGGA 780
DB 721 GGCCTGTTCTCCATCAACGAGGAAATATAGATCAAAACAAAGGAGAAAGTCTCTGGA 780
QY 781 GCTGTCAGAGCCCTTGTCTTACAGCTGCCCCAGGGAGGAGGGCAGCACCATCCCAT 840
DB 781 GCTGTCAGAGCCCTTGTCTGTTTACAGCTGCCCCAGGGAGGAGGGCAGCACCATCCCAT 840
QY 841 CCAGGAGGATTACCGAAAACCGGAGCTGCTGCTCCCTGAGCCAGCACCTGCGGTAG 900
DB 841 CCAGGAGGATTACCGAAAACCGGAGCTGCTGCTCCCTGAGCCAGCACCTGCGGTAG 900
QY 901 CTGCACTACAGCCCTGGCCCTCCACCCCGCCAGCCATCCAAAGGAGAGTGTGAGACC 960
DB 901 CTGCACTACAGCCCTGGCCCTCCACCCCGCCAGCCATCCAAAGGAGAGTGTGAGACC 960
QY 961 TGGCAGCCACAATGTCAGTCCCCTCTTGTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
DB 961 TGGCAGCCACAATGTCAGTCCCCTCTTGTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
QY 1021 GAGTGTCTTTTCGAGACTGCGAGGACGAGGACAAATATGTGATGAGTGTGAGTGGGAA 1080
DB 1021 GAGTGTCTTTTCGAGACTGCGAGGACGAGGACAAATATGTGATGAGTGTGAGTGGGAA 1080
QY 1081 GCAGGAGCCAGCCAGCTGCGCGCGG-TGCAGGAGGGGGGGCTCTGTTGTAAAGCA 1139
DB 1081 GCAGGAGCCAGCCAGCTGCGCGCGG-TGCAGGAGGGGGGGCTCTGTTGTAAAGCA 1140
QY 1140 CACTTCTGTGCGAAAGACCCACATGCTACAGAGCGGGCAAAATAAAGTGACAGATGAC 1199
DB 1141 CACTTCTGTGCGAAAGACCCACATGCTACAGAGCGGGCAAAATAAAGTGACAGATGAC 1200
QY 1200 C 1200
DB 1201 C 1201

RESULT 15
ADQ23741
ID ADQ23741 standard; DNA; 1711 BP.
XX
AC ADQ23741;
XX
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6561.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW db.
XX
OS
XX Homo sapiens.
XX

